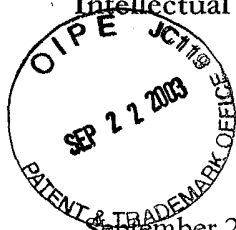


1617
SEED

Intellectual Property Law Group PLLC



September 22, 2003

Attn: Legal Assistants
Art Unit 1617
U.S. Patent and Trademark Office
P.O. Box 1450
Alexandria, VA 22313-1450

701 Fifth Avenue, Suite 6300
Seattle WA 98104-7092 USA
Facsimile: (206) 682-6031
Telephone: (206) 622-4900
www.seedlaw.com

Jeffrey C. Pepe, Ph.D.
Patent Attorney
jeffp@seedlaw.com

SEP 25 2003

RECEIVED

FOH CENTER 1600/2900

To whom it may concern:

We herewith return the enclosed Amendment Checklist papers and attached claims, which appear to have been inadvertently placed within the Office Action sent to our office on September 15, 2003 for U.S. Patent Application No. 08/486,867.

These Checklists, referring to U.S. Application Nos. 10/077,588 and 09/697,123, do not correspond to the application to which the Office Action referred, nor are they applications being prosecuted by our firm.

If you have any questions or require additional information, please call.

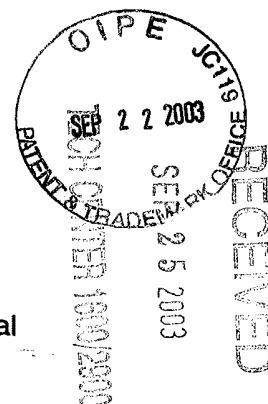
Sincerely,
SEED Intellectual Property Law Group PLLC

Linda Povinelli
For Jeffrey C. Pepe

Enclosures: As noted

(JCP:imp)

418151



1. (Amended) A DNA fragment which has a sequence selected from the group consisting of SEQ ID NOS:1 to 4 and 6 to 24.
2. (Amended) A method for identifying the species or subspecies of a mycobacterial strain comprising the steps of:
 - a) digesting a DNA fragment which has a sequence selected from the group consisting SEQ ID NO:1 to SEQ ID NO:24 with at least one restriction enzyme selected from the group consisting of *HaeIII*, *MspI*, *Sau3AI*, and *BstEII* to obtain a first DNA fragment length polymorphism pattern;
 - b) isolating a DNA fragment from the mycobacterial strain to be identified;
 - c) amplifying *rpoB* region of the DNA fragment isolated in step (b), said amplification being performed by using a primer of SEQ ID NO: 15 or SEQ ID NO: 26;
 - d) digesting the DNA fragment amplified in step c) with the at least one restriction enzyme employed in step a) to obtain a second DNA fragment length polymorphism pattern; and
 - e) comparing the first DNA fragment length polymorphism pattern obtained in step a) with the second DNA fragment length polymorphism pattern obtained in step d), thereby identifying the species or subspecies of a mycobacterial strain.
3. (Amended) A method of claim 2, wherein said first and second DNA fragment length polymorphism by electrophoresis.
5. (Amended) A method of claim 2, wherein said mycobacterial strain is selected from the group consisting of *M. tuberculosis*, *M. avium*, *M. abscessus*, *M. flavescens*, *M. africanum*, *M. bovis*, *M. chelonae*, *M. celatum*, *M. fortuitum*, *M. gordonae*, *M. gastri*, *M. haemophilum*, *M. intracellulare*, *M. kansasii*, *M. mageritensis*, *M. marinum*, *M. szulgai*, *M. terrae*, *M. scrofulaceum*, *M. ulcerans*, and *M. xenopi*.

IN THE DRAWINGS

Corrected Figs. 6a-6b are attached.